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☐ 1: CAA54576. N2042 [Saccharomy...[gi:496725]

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LOCUS CAA54576 661 aa .linear PLN 24-MAY-1995  
DEFINITION N2042 [Saccharomyces cerevisiae].  
ACCESSION CAA54576  
VERSION CAA54576.1 GI:496725  
DBSOURCE embi locus SCN201952, accession X77395.1  
KEYWORDS

SOURCE Saccharomyces cerevisiae (baker's yeast)  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1  
AUTHORS Verhasselt, P., Aert, R., Voet, M. and Volckaert, G.  
TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking  
the centromere on the Saccharomyces cerevisiae chromosome XIV right  
arm

JOURNAL Yeast 10 (10), 1355-1361 (1994)

MEDLINE 95208356

PUBMED 7900425

REFERENCE 2 (residues 1 to 661)

AUTHORS Volckaert, G.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene  
Technology, Catholic University of Leuven, W. Decrolyaan 42, 3001  
Leuven, BELGIUM

FEATURES Location/Qualifiers  
source 1..661  
/organism="Saccharomyces cerevisiae"  
/strain="FY1679"  
/db\_xref="taxon:4932"  
/chromosome="XIV"  
/map="centromeric region (right arm)"  
/clone="cosmid 14-20"  
/clone\_lib="B. Dujon (Paris)"

Protein 1..661  
/name="N2042"

CDS 1..661  
/gene="N2042"  
/coded\_by="X77395.1:11755..13740"  
/db\_xref="GOA:P40345"  
/db\_xref="SGD:S0005291"  
/db\_xref="SWISS-PROT:P40345"

#### ORIGIN

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121 ylddwkdvlp qgissfiddi qagnystssl ddlsenfavg kqlrldynie akhpvvmvpg
181 vistgieswg vigddecdss ahfrkrlwgs fymrltmvmd kvcwlkhvml dpetglppn
241 ftlraaggfe stdyfiagyw iwnkvfqnlg vigyepnkmt saaydwrlay ldlerdryf
301 tkлкеqielf hqlsgkvcl ighsmgsqii fyfmkwveae gplyngggrg wvnehidsfi
361 naagtllgap kavpalisge mkdtiqlntl amyglekffs rierkvmlqt wggipsmlpk
421 geeviwgdmk sssedalnnn tdygnfirf erntsdafnk nltmkdainm tllsispewlq
481 rrvheqysfg yskneeelrk nelhhkhswn pmevplpeap hmkiyciygv nnptarayvy
541 keeddssaln ltidyekqp vfltegdgtv plvahsmchk waqgaspynp aginvtivem
601 khqpdrfdir ggaksaehvd ilgsaelndy ilkiasgngd lveprqlsnl sqwvsqmpfp
661 m
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//

Sep 16 2003 13:15:10

# DNA is known in yeast

LOCUS SCN201952 23901 bp DNA linear PLN 24-MAY-1995  
 DEFINITION S.cerevisiae N2019, N2021, N2023, N2025, N2027, N2031, N2048 and N2050 genes.  
 ACCESSION X77395  
 VERSION X77395.1 GI:496717  
 KEYWORDS mitochondrial citrate synthase; PRP2 gene; RNA polymerase III; RNA-dependent ATPase; rpc34 gene; tau34 protein; tRNA-Asn; tRNA-Pro; uridine kinase; URK1 gene; yun34 gene.  
 SOURCE Saccharomyces cerevisiae.  
 ORGANISM Saccharomyces cerevisiae  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 REFERENCE 1 (bases 1 to 23901)  
 AUTHORS Verhasselt, P., Aert, R., Voet, M. and Volckaert, G.  
 TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right arm  
 JOURNAL Yeast 10 (10), 1355-1361 (1994)  
 REFERENCE 2 (bases 1 to 23901)  
 AUTHORS Volckaert, G.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven, W. Decrolyaan 42, 3001 Leuven, BELGIUM

Query Match 100.0%; Score 1986; DB 8; Length 23901;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCACACTGTTTCGAAGAAATGTCCAGAACCAAAGAGTGATTCTGATGAAAACAAT 60  
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 Db 11755 ATGGGCACACTGTTTCGAAGAAATGTCCAGAACCAAAGAGTGATTCTGATGAAAACAAT 11814  
 Qy 61 AAAGGGGGTTCTGTTTCATAACAAGCGAGAGAGCAGAAACCACATTCATCATCAACAGGGA 120  
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 Db 11815 AAAGGGGGTTCTGTTTCATAACAAGCGAGAGAGCAGAAACCACATTCATCATCAACAGGGA 11874  
 Qy 121 TTAGGCCATAAGAGAAGAAGGGGTATTAGTGGCAGTGCAAAAAGAAATGAGCGTGGCAAA 180  
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 Qy 241 ATTTTCATTCTTGGTGCATTCTTAGGTGTACTTTTGCCGTTTAGCTTTGGCGCTTATCAT 300  
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Qy	481	AAACAACCTCTTACGTGATTATAATATCGAGGCCAAACATCCTGTTGTAATGGTTCCTGGT	540
Db	12235	AAACAACCTCTTACGTGATTATAATATCGAGGCCAAACATCCTGTTGTAATGGTTCCTGGT	12294
Qy	541	GTCATTTCTACGGGAATTGAAAGCTGGGGAGTTATTGGAGACGATGAGTGCGATAGTTCT	600
Db	12295	GTCATTTCTACGGGAATTGAAAGCTGGGGAGTTATTGGAGACGATGAGTGCGATAGTTCT	12354
Qy	601	GCGCATTTTCGTAAACGGCTGTGGGGAAGTTTTTACATGCTGAGAACAATGGTTATGGAT	660
Db	12355	GCGCATTTTCGTAAACGGCTGTGGGGAAGTTTTTACATGCTGAGAACAATGGTTATGGAT	12414
Qy	661	AAAGTTTGTTGGTTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	720
Db	12415	AAAGTTTGTTGGTTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	12474
Qy	721	TTTACGCTACGTGCAGCACAGGGCTTCGAATCAACTGATTATTTTCATCGCAGGGTATTGG	780
Db	12475	TTTACGCTACGTGCAGCACAGGGCTTCGAATCAACTGATTATTTTCATCGCAGGGTATTGG	12534
Qy	781	ATTTGGAACAAAGTTTTCCAAAATCTGGGAGTAATTGGCTATGAACCCAATAAAATGACG	840
Db	12535	ATTTGGAACAAAGTTTTCCAAAATCTGGGAGTAATTGGCTATGAACCCAATAAAATGACG	12594
Qy	841	AGTGCTGCGTATGATTGGAGGCTTGCATATTTAGATCTAGAAAGACGCGATAGGTACTTT	900
Db	12595	AGTGCTGCGTATGATTGGAGGCTTGCATATTTAGATCTAGAAAGACGCGATAGGTACTTT	12654
Qy	901	ACGAAGCTAAAGGAACAAATCGAACTGTTTCATCAATTGAGTGGTGAAAAAGTTTGTTTA	960
Db	12655	ACGAAGCTAAAGGAACAAATCGAACTGTTTCATCAATTGAGTGGTGAAAAAGTTTGTTTA	12714
Qy	961	ATTGGACATTCTATGGGTTCTCAGATTATCTTTTACTTTATGAAATGGGTCGAGGCTGAA	1020
Db	12715	ATTGGACATTCTATGGGTTCTCAGATTATCTTTTACTTTATGAAATGGGTCGAGGCTGAA	12774
Qy	1021	GGCCCTCTTTACGGTAATGGTGGTTCGTGGCTGGGTTAACGAACACATAGATTCATTCATT	1080
Db	12775	GGCCCTCTTTACGGTAATGGTGGTTCGTGGCTGGGTTAACGAACACATAGATTCATTCATT	12834
Qy	1081	AATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGGCAGTTCAGCTCTAATTAGTGGTGAA	1140
Db	12835	AATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGGCAGTTCAGCTCTAATTAGTGGTGAA	12894
Qy	1141	ATGAAAGATACCATTCGAATTAAATACGTTAGCCATGTATGGTTTGAAAAGTTCTTCTCA	1200
Db	12895	ATGAAAGATACCATTCGAATTAAATACGTTAGCCATGTATGGTTTGAAAAGTTCTTCTCA	12954
Qy	1201	AGAATTGAGAGAGTAAAAATGTTACAAACGTGGGGTGGTATACCATCAATGCTACCAAAG	1260
Db	12955	AGAATTGAGAGAGTAAAAATGTTACAAACGTGGGGTGGTATACCATCAATGCTACCAAAG	13014

Qy	1261	GGAGAAGAGGTCATTTGGGGGGATATGAAGTCATCTTCAGAGGATGCATTGAATAACAAC	1320
Db	13015	GGAGAAGAGGTCATTTGGGGGGATATGAAGTCATCTTCAGAGGATGCATTGAATAACAAC	13074
Qy	1321	ACTGACACATACGGCAATTTTCATTCGATTTGAAAGGAATACGAGCGATGCTTTCAACAAA	1380
Db	13075	ACTGACACATACGGCAATTTTCATTCGATTTGAAAGGAATACGAGCGATGCTTTCAACAAA	13134
Qy	1381	AATTTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCCAA	1440
Db	13135	AATTTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCCAA	13194
Qy	1441	AGAAGAGTACATGAGCAGTACTCGTTCGGCTATTCCAAGAATGAAGAAGAGTTAAGAAAA	1500
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Qy	1501	AATGAGCTACACCACAAGCACTGGTCTGAATCCAATGGAAGTACCACTTCCAGAAGCTCCC	1560
Db	13255	AATGAGCTACACCACAAGCACTGGTCTGAATCCAATGGAAGTACCACTTCCAGAAGCTCCC	13314
Qy	1561	CACATGAAAATCTATTGTATATACGGGGTGAACAACCCAACTGAAAGGGCATATGTATAT	1620
Db	13315	CACATGAAAATCTATTGTATATACGGGGTGAACAACCCAACTGAAAGGGCATATGTATAT	13374
Qy	1621	AAGGAAGAGGATGACTCCTCTGCTCTGAATTTGACCATCGACTACGAAAGCAAGCAACCT	1680
Db	13375	AAGGAAGAGGATGACTCCTCTGCTCTGAATTTGACCATCGACTACGAAAGCAAGCAACCT	13434
Qy	1681	GTATTCCTCACCGAGGGGGACGGAACCGTTCGGCTCGTGGCGCATTC AATGTGTACAAA	1740
Db	13435	GTATTCCTCACCGAGGGGGACGGAACCGTTCGGCTCGTGGCGCATTC AATGTGTACAAA	13494
Qy	1741	TGGGCCCAGGGTGCTTCACCGTACAACCCTGCCGGAATTAACGTTACTATTGTGGAAATG	1800
Db	13495	TGGGCCCAGGGTGCTTCACCGTACAACCCTGCCGGAATTAACGTTACTATTGTGGAAATG	13554
Qy	1801	AAACACCAGCCAGATCGATTTGATATACGTGGTGGAGCAAAAAGCGCCGAACACGTAGAC	1860
Db	13555	AAACACCAGCCAGATCGATTTGATATACGTGGTGGAGCAAAAAGCGCCGAACACGTAGAC	13614
Qy	1861	ATCCTCGGCAGCGCGGAGTTGAACGATTACATCTTGAAAATTGCAAGCGGTAATGGCGAT	1920
Db	13615	ATCCTCGGCAGCGCGGAGTTGAACGATTACATCTTGAAAATTGCAAGCGGTAATGGCGAT	13674
Qy	1921	CTCGTCGAGCCACGCCAATTGTCTAATTTGAGCCAGTGGGTTTCTCAGATGCCCTTCCCA	1980
Db	13675	CTCGTCGAGCCACGCCAATTGTCTAATTTGAGCCAGTGGGTTTCTCAGATGCCCTTCCCA	13734
Qy	1981	ATGTAA	1986
Db	13735	ATGTAA	13740